

K. Canella

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/225,080

DATE: 06/13/2000
TIME: 03:00:50

INPUT SET: S35618.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Au-Young, Janice
6
7 (ii) TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
8
9 (iii) NUMBER OF SEQUENCES: 26
10
11 (iv) CORRESPONDENCE ADDRESS:
12 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
13 (B) STREET: 3174 Porter Drive
14 (C) CITY: Palo Alto
15 (D) STATE: CA
16 (E) COUNTRY: U.S.
17 (F) ZIP: 94304
18
19 (v) COMPUTER READABLE FORM:
20 (A) MEDIUM TYPE: Diskette
21 (B) COMPUTER: IBM Compatible
22 (C) OPERATING SYSTEM: DOS
23 (D) SOFTWARE: FastSEQ Version 1.5
24
25 (vi) CURRENT APPLICATION DATA:
26 (A) APPLICATION NUMBER: 09/225,080
27 (B) FILING DATE:
28
29 (vii) PRIOR APPLICATION DATA:
30 (A) APPLICATION NUMBER: US/08/675,508
31 (B) FILING DATE:
32
33 (viii) ATTORNEY/AGENT INFORMATION:
34 (A) NAME: Billings, Lucy J.
35 (B) REGISTRATION NUMBER: 36,749
36 (C) REFERENCE/DOCKET NUMBER: PF-0066 US
37
38 (ix) TELECOMMUNICATION INFORMATION:
39 (A) TELEPHONE: 415-855-0555
40 (B) TELEFAX: 415-845-4166
41
42 (2) INFORMATION FOR SEQ ID NO:1:
43
44 (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 131 amino acids
46 (B) TYPE: amino acid

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47 (C) STRANDEDNESS: single
48 (D) TOPOLOGY: linear
49
50 (ii) MOLECULE TYPE: peptide
51
52 (vii) IMMEDIATE SOURCE:
53 (A) LIBRARY: SCAH-1
54 (B) CLONE:
55
56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
57
58 Met Lys Ile Phe Leu Pro Val Leu Leu Ala Ala Leu Leu Gly Val Glu
59 1 5 10 15
60 Arg Ala Ser Ser Leu Met Cys Phe Ser Cys Leu Asn Gln Lys Ser Asn
61 20 25 30
62 Leu Tyr Cys Leu Lys Pro Thr Ile Cys Ser Asp Gln Asp Asn Tyr Cys
63 35 40 45
64 Val Thr Val Ser Ala Ser Ala Gly Ile Gly Asn Leu Val Thr Phe Gly
65 50 55 60
66 His Ser Leu Ser Lys Thr Cys Ser Pro Ala Cys Pro Ile Pro Glu Gly
67 65 70 75 80
68 Val Asn Val Gly Val Ala Ser Met Gly Ile Ser Cys Cys Gln Ser Phe
69 85 90 95
70 Leu Cys Asn Phe Ser Ala Ala Asp Gly Gly Leu Arg Ala Ser Val Thr
71 100 105 110
72 Leu Leu Gly Ala Gly Leu Leu Leu Ser Leu Xaa Pro Ala Leu Leu Arg
73 115 120 125
74 Phe Gly Pro
75 130
76

77 (2) INFORMATION FOR SEQ ID NO:2:
78
79 (i) SEQUENCE CHARACTERISTICS:
80 (A) LENGTH: 123 amino acids
81 (B) TYPE: amino acid
82 (C) STRANDEDNESS: single
83 (D) TOPOLOGY: linear
84
85 (ii) MOLECULE TYPE: peptide
86
87 (vii) IMMEDIATE SOURCE:
88 (A) LIBRARY: SCAH-2
89 (B) CLONE:
90
91 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
92
93 Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln
94 1 5 10 15
95 Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn
96 20 25 30
97 Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys
98 35 40 45
99 Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys

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100          50          55          60
101 Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly
102 65          70          75          80
103 Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys Asn Xaa Ser Gly
104          85          90          95
105 Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala
106          100          105          110
107 Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu
108          115          120
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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SCAH-1
- (B) CLONE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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126 NAGGANGGTG GGGGACCCAN GGGTCCAGAG CGCAGTTCGG GTCGGAGCTY CGWCCAGGCT 60
127 GCTGGTACCT GCGTCCGCCC GGCGAGCAGG ACAGGCTGCT TTGGTTTG TG ACCTCCAGGC 120
128 AGGACGGCCA TCCTCTCCAG AATGAAGATC TTCTTGCCAG TGCTGCTGGC TGCCCTTCTG 180
129 GGTGTGGAGC GAGCCAGCTC GCTGATGTGC TTCTCTGCT TGAACCAGAA GAGCAATCTG 240
130 TACTGCCTGA AGCCGACCAT CTGCTCCGAC CAGGACAACT ACTGCGTGAC TGTGTCTGCT 300
131 AGTGCCGGCA TTGGGAATCT CGTGACATTT GGCCACAGCC TGAGCAAGAC CTGTTCCCCG 360
132 GCCTGCCCCA TCCAGAAAGG CGTCAATGTT GGTGTGGCTT CCATGGGCAT CAGCTGCTGC 420
133 CAGAGCTTTC TGTGCAATTT CAGTGC GGCC GATGGCGGGC TGCGGGCAAG CGTCACCTG 480
134 CTGGGTGCCG GGCTGCTGCT GAGCCTGWTG CCGGCCCTGC TGCGGTTTGG CCCCTGA 537

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SCAH-2
- (B) CLONE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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152 GTGACCATGA AGGCTGTGCT GCTTGCCCTG TTGATGGCAG GCTTGGCCCT GCAGCCAGGC 60

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153 ACTGCCCTGC TGTGCTACTC CTGCAAAGCC CAGGTGAGCA ACGAGGACTG CCTGCAGGTG 120
154 GAGAACTGCA CCCAGCTGGG GGAGCAGTGC TGGACCGCGC GCATCCGCGC AGTTGGCCTC 180
155 CTGACCGTCA TCAGCAAAGG CTGCAGCTTG AACTGCGTGG ATGACTCACA GGACTACTAC 240
156 GTGGGCAAGA AGAACATCAC GTGCTGTGAC ACCGACTTGT GCAACGSCAG CGGGGCCCCAT 300
157 GCCCTGCAGC CGGCTGCCGC CATCCTTGCG CTGCTCCCTG CACTCGGCCT GCTGCTCTGG 360
158 GGACCCGGCC AGCTATAGGC TCTGGGGGGC CCCGMTGCAG CCCACACTGG GTGTGGTGCC 420
159 CCAAGGCCTC TGTGSCACTC CTMACAGACC TGGGCCCAGT GGGAGSCTGT CTCTNGGTTC 480
160 CTGAGGCACA TCCT 494

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 434660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

178 Met Ser Ala Thr Ser Asn Met Arg Val Phe Leu Pro Val Leu Leu Ala
179   1           5           10           15
180 Ala Leu Leu Gly Met Glu Gln Val His Ser Leu Met Cys Phe Ser Cys
181       20           25           30
182 Thr Asp Gln Lys Asn Asn Ile Asn Cys Leu Trp Pro Val Ser Cys Gln
183       35           40           45
184 Glu Lys Asp His Tyr Cys Ile Thr Leu Ser Ala Ala Gly Phe Gly
185       50           55           60
186 Asn Val Asn Leu Gly Tyr Thr Leu Asn Lys Gly Cys Ser Pro Ile Cys
187       65           70           75           80
188 Pro Ser Glu Asn Val Asn Leu Asn Leu Gly Val Ala Ser Val Asn Ser
189       85           90           95
190 Tyr Cys Cys Gln Ser Ser Phe Cys Asn Phe Ser Ala Ala Gly Leu Gly
191       100          105          110
192 Leu Arg Ala Ser Ile Pro Leu Leu Gly Leu Gly Leu Leu Ser Leu
193       115          120          125
194 Leu Ala Leu Leu Gln Leu Ser Pro
195       130          135

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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206
207 (vii) IMMEDIATE SOURCE:
208 (A) LIBRARY: GenBank
209 (B) CLONE: 1199651
210
211 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
212
213 Met Ser Thr Thr Ser Ser Met Arg Val Phe Ser Ile Val Leu Gln Ala
214 1 5 10 15
215 His Leu Leu Gly Val Glu Leu Val Pro Ser Leu Ile Cys Ser Ser Cys
216 20 25 30
217 Thr His Gln Lys Ser Asn Ile Asn Pro Pro Trp Pro Val Ala Cys Lys
218 35 40 45
219 Asp Thr Gly Asn Tyr Cys Ile Met Leu Phe Ser Ala Val Gly Phe Gly
220 50 55 60
221 Asn Val Asn Leu Gly Tyr Thr Leu Asn Thr Gly Cys Ser Gln Ser Cys
222 65 70 75 80
223 Pro His Glu Asn Ile Asn Ile Asn Pro Gly Val Ala Ser Val Asn Ser
224 85 90 95
225 Tyr Gln Ser Ser Phe Cys Asn Phe Ser Asn Ala Cys Leu
226 100 105
227

(2) INFORMATION FOR SEQ ID NO:7:

228
229
230 (i) SEQUENCE CHARACTERISTICS:
231 (A) LENGTH: 148 base pairs
232 (B) TYPE: nucleic acid
233 (C) STRANDEDNESS: single
234 (D) TOPOLOGY: linear
235

236 (ii) MOLECULE TYPE: cDNA
237

238 (vii) IMMEDIATE SOURCE:
239 (A) LIBRARY: THP1PEB01
240 (B) CLONE: 72518
241

242 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
243

244 CCTGAAGCCG ACCATCTGNT CCGACCAGGN CAACTACTGN GTGACTGTGT CTGCTAGTGC 60
245 CGGCATTTGG AATCTTGTGC CATTNGACA CAGCCTNAGC AAGACCTNTT CCCCAGCCTN 120
246 NCCCATCCCA GAAGGNGTCA ATNATNGT 148
247

(2) INFORMATION FOR SEQ ID NO:8:

248
249
250 (i) SEQUENCE CHARACTERISTICS:
251 (A) LENGTH: 196 base pairs
252 (B) TYPE: nucleic acid
253 (C) STRANDEDNESS: single
254 (D) TOPOLOGY: linear
255

256 (ii) MOLECULE TYPE: cDNA
257

258 (vii) IMMEDIATE SOURCE:

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SEQUENCE VERIFICATION REPORT
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Original Text